Phosphorylation of Synaptic GTPase Activating Protein (synGAP) by Ca^{2+}/calmodulin-dependent protein kinase II (CaMKII) and cyclin-dependent kinase 5 (CDK5) alters the ratio of its GAP activity toward Ras and Rap GTPases*

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*Running title: *Distinct regulation of Ras and Rap GAP activities of synGAP*

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SUPPLEMENTARY TABLE 1. *CaMKII and CDK5 Phosphorylation Sites in R-synGAP*

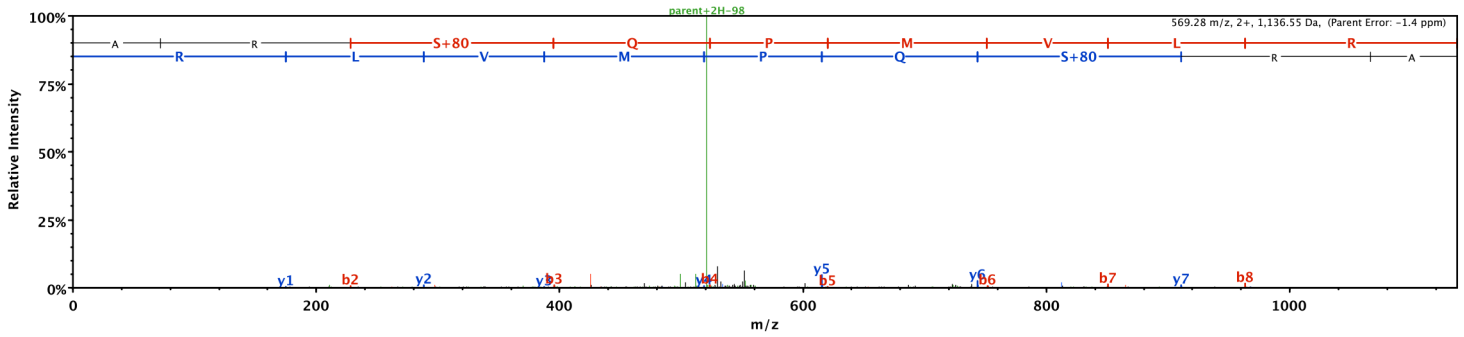
CaMKII and CDK5 phosphorylation sites in r-synGAP detected by mass spectrometry as described under methods. MS2 and MS3 spectra corresponding to each tryptic peptide are contained in the accompanying pdf file. When several unique peptides were detected for a single phosphorylation site, we have shown only the peptide with the lowest predicted false localization rate.

Phosphorylated Residue	Kinase	Peptide Sequence (Modified Residue(s) in Lower Case)	Mascot Ion Score	Mascot Delta Score	False Localization Rate
S728	CDK5	(R)ARsQPMVLR(G)	42.6	42.6	0.0%
S773	CDK5	(R)LPsPTKEKPPPPPPGGGK(D)	55.6	14.6	0.4%
T775	CDK5	(R)GLNSSmDMARLPSPtK(E)	51.8	9.8	1.4%
S802	CDK5	(R)SsPAYcTSSSDITEPEQK(M)	84.5	0	>17%
S842	CDK5	(R)LNsSSVSNLAAVGDLLHSSQASLTAALGLRPAPAGR(L)	116.3	12.7	0.7%
S728	CaMKII	(R)ARsQPMVLR(G)	36	36	0.0%
S737	CaMKII	(R)GPsAEMQGYMMR(D)	70.9	70.9	0.0%
S750	CaMKII	(R)DLNsSIDLQSFmAR(G)	48.3	1.7	11.0%
S751	CaMKII	(R)DLNSsIDLQSFmAR(G)	83.7	17.2	0.2%
S756	CaMKII	(R)DLNSsIDLQsFmAR(G)	50.1	0	>17%
S764	CaMKII	(R)GLNsSMDMARLPSPTK(E)	55.7	2.2	9.5%
S765	CaMKII	(R)GLNSsMDMAR(L)	52.5	14	0.5%

Phosphorylated Residue	Kinase	Peptide Sequence (Modified Residue(s) in Lower Case)	Mascot Ion Score	Mascot Delta Score	False Localization Rate
S808	CaMKII	(R)SSPAYcTsSSDITEPEQK(M)	44.2	3.7	6.4%
S809	CaMKII	(R)SSPAYcTSsSDITEPEQK(M)	47.5	5.6	4.0%
S810	CaMKII	(R)SSPAYcTSSsDITEPEQK(M)	46.9	0	>17%
S821	CaMKII	(K)MLsVNKSVSMLDLQGDGPGGR(L)	66.4	13.9	0.5%
S825	CaMKII	(K)mLSVNKsVSMLDLQGDGPGGR(L)	85	25.2	0.0%
S827	CaMKII	(K)SVsMLDLQGDGPGGR(L)	92.6	22	0.1%
S842	CaMKII	(R)LNsSSVSNLAAVGDLLHSSQASLTAALGLRPAPAGR(L)	84.1	10.2	1.2%
S843	CaMKII	(R)LNSsSVSNLAAVGDLLHSSQASLTAALGLRPAPAGR(L)	75	0	>17%
S882	CaMKII	(R)LSQGSGsSITAAGmR(L)	70.4	13	0.6%
S883	CaMKII	(R)LSQGSGSsITAAGMR(L)	83	15	0.4%
T885	CaMKII	(R)LSQGSGSSItAAGmR(L)	56.4	13.8	0.5%
S892	CaMKII	(R)LSQGSGSSITAAGMRLsQmGVtTDGVPAQQLR(I)	44.5	18.4	0.2%
T897	CaMKII	(R)LSQMGVtTDGVPAQQLR(I)	92.6	18.4	0.2%
T898	CaMKII	(R)LSQmGVTtDGVPAQQLR(I)	85.1	0	>17%
S990	CaMKII	(K)SEDLSTGVPKPPAASILHSHsYSDEFGPSGTDFTR(R)	41	6.8	2.9%
S1093	CaMKII	(R)QQsLsKEGSIGGSGGSGGGGGGGLKPSITK(Q)	32.9	13.6	0.5%
S1095	CaMKII	(R)QQsLsKEGSIGGSGGSGGGGGGGLKPSITK(Q)	32.9	13.6	0.5%
S1099	CaMKII	(K)EGsIGGsGGSGGGGGGGLKPSITK(Q)	42.6	37.6	0.0%
S1123	CaMKII	(K)QHsQTPSTLNPTmPASER(T)	73.7	33.9	0.0%
S1150	CaMKII	(R)TVAWVSNMPHLsADIESAHIEREEYK(L)	58	26.4	0.0%
S1171	CaMKII	(K)LKEYSKsMDESRLDR(V)	38.6	17.2	0.2%
S1210	CaMKII	(R)RLLsQEEQTSK(I)	54.3	39.8	0.0%
S1283	CaMKII	(R)GsFPPWVQQTRV(-)	74.1	69.9	0.0%
T1291	CaMKII	(R)LLDAQRGsFPPWVQQtRV(-)	31.5	31.5	0.0%

CaMKII S728

MS2



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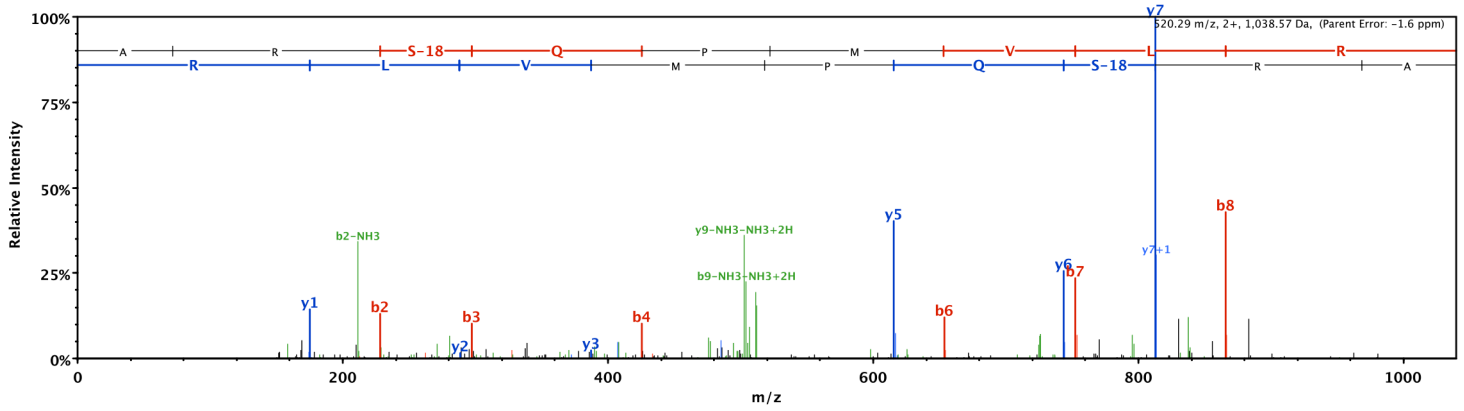

CaMKII S737

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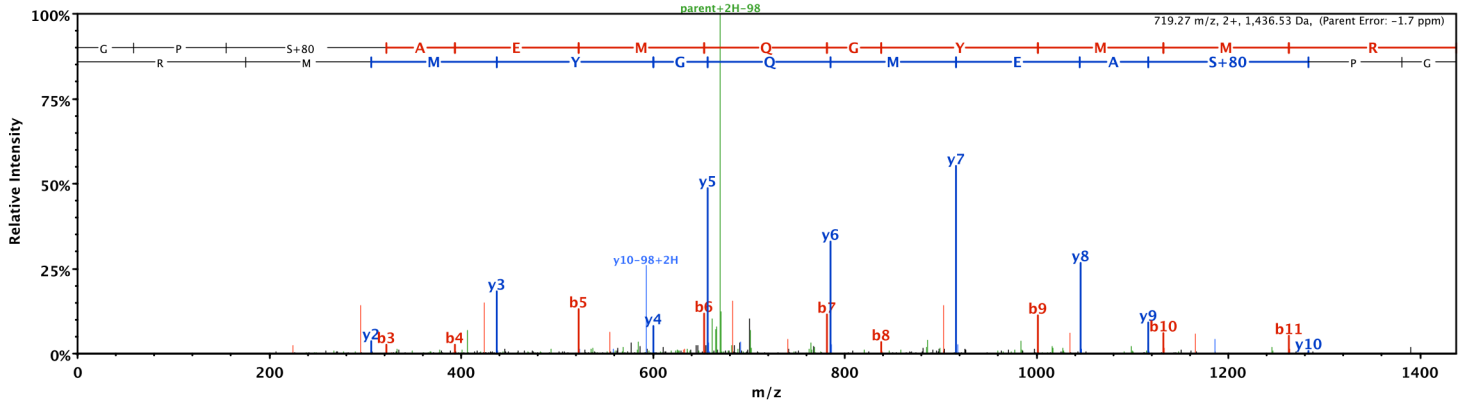

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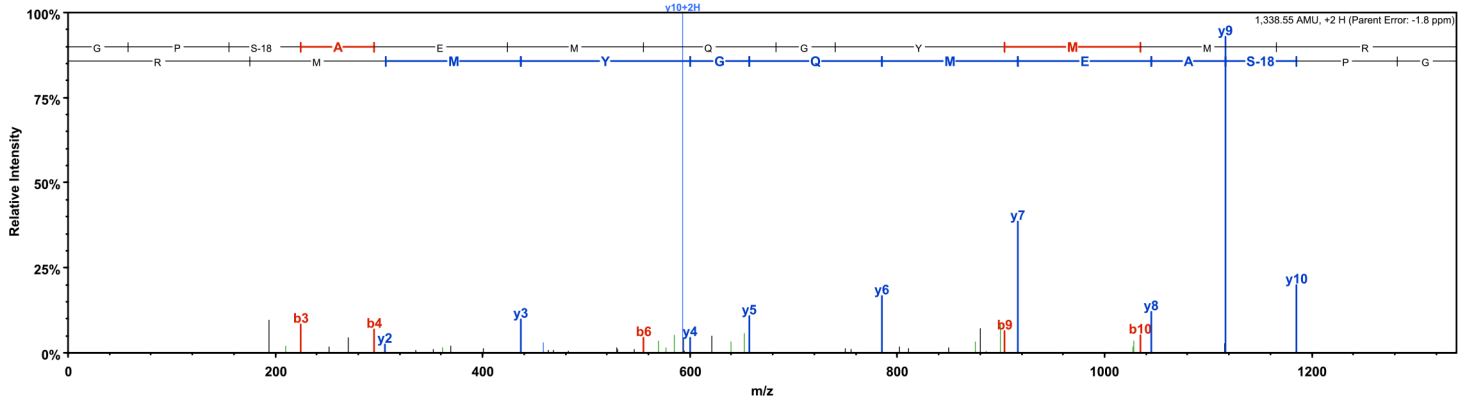

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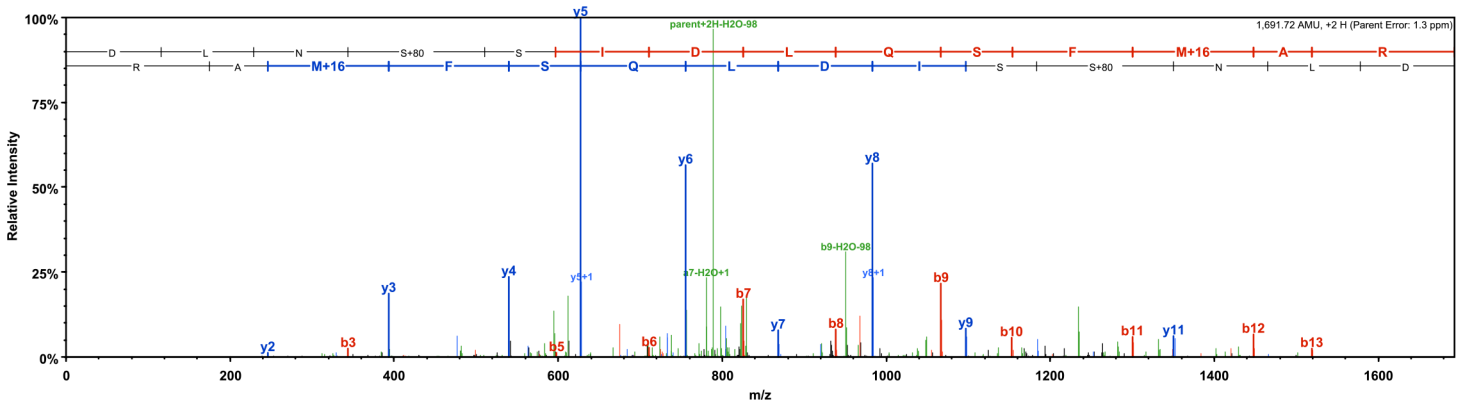

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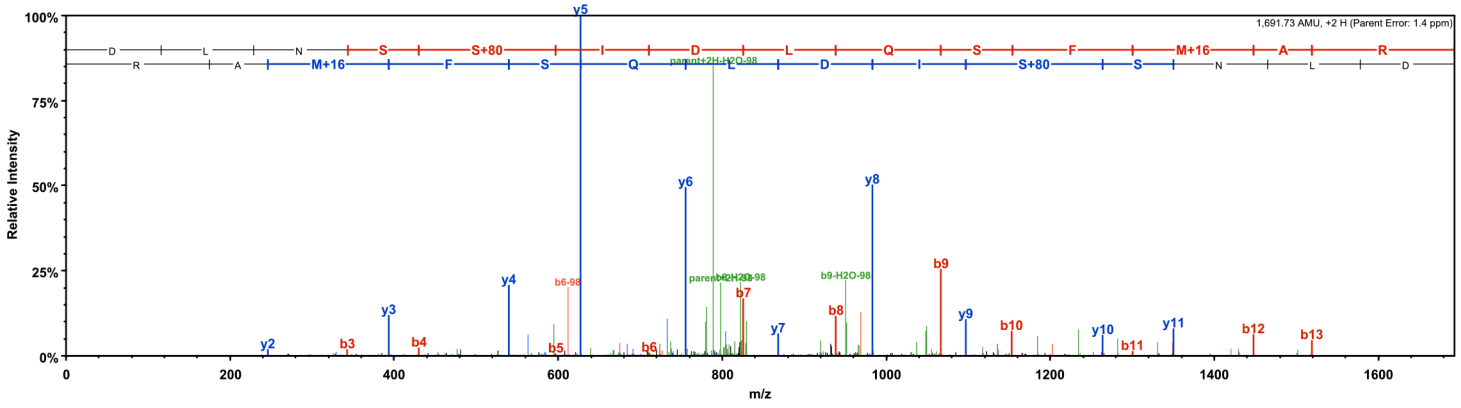

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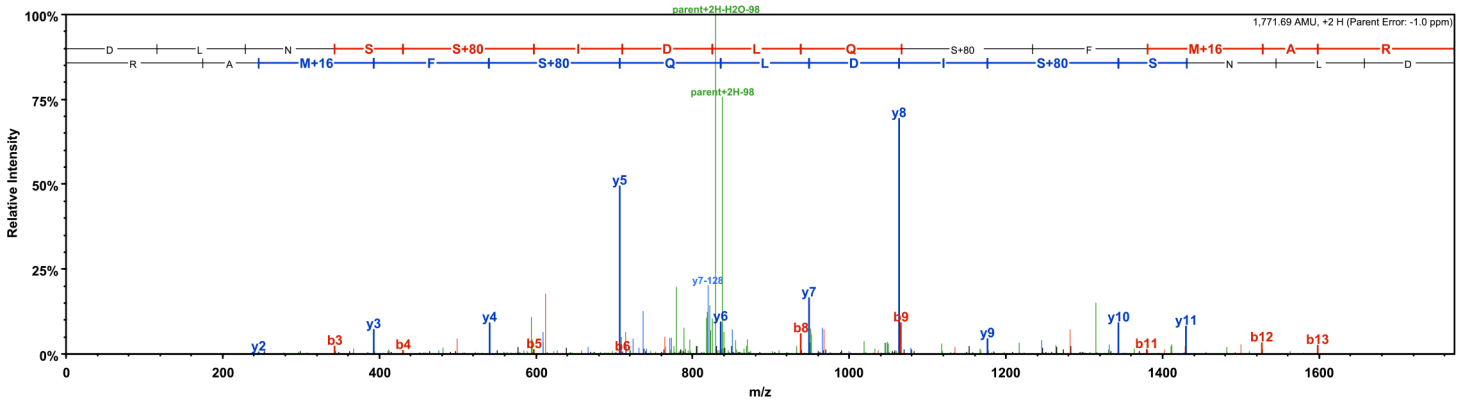

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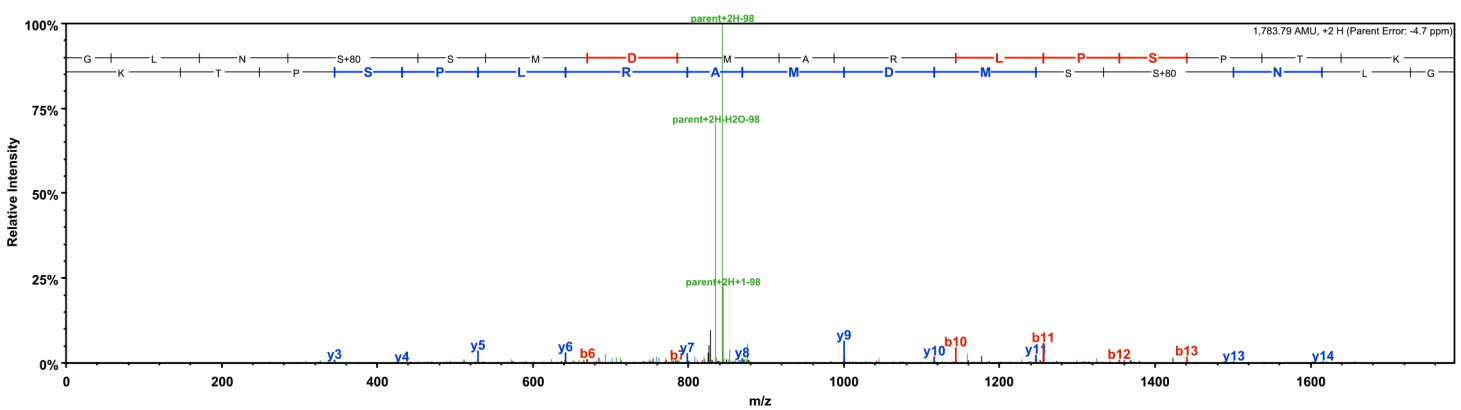

CaMKII S765

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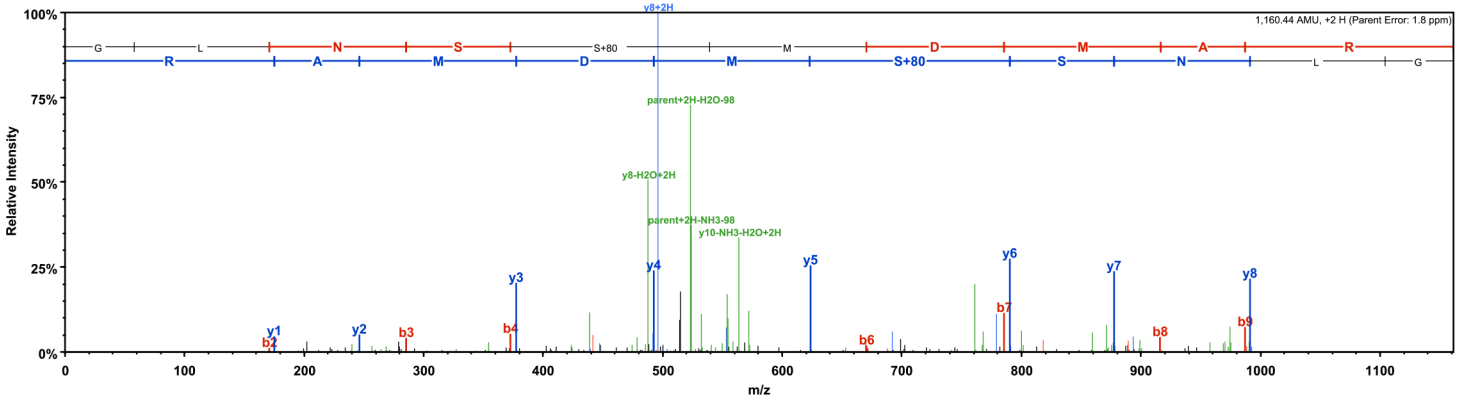

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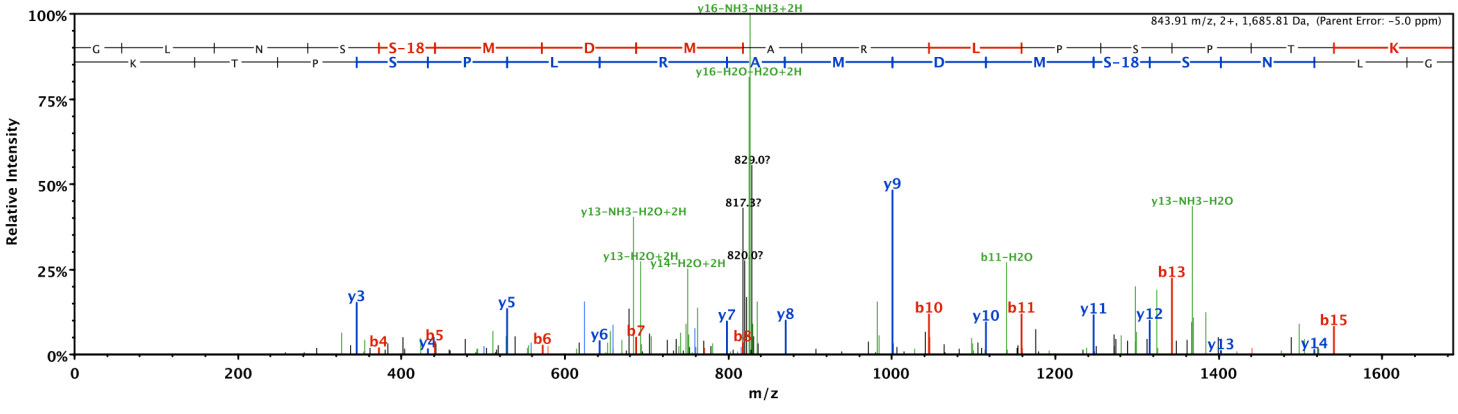

CaMKII S808

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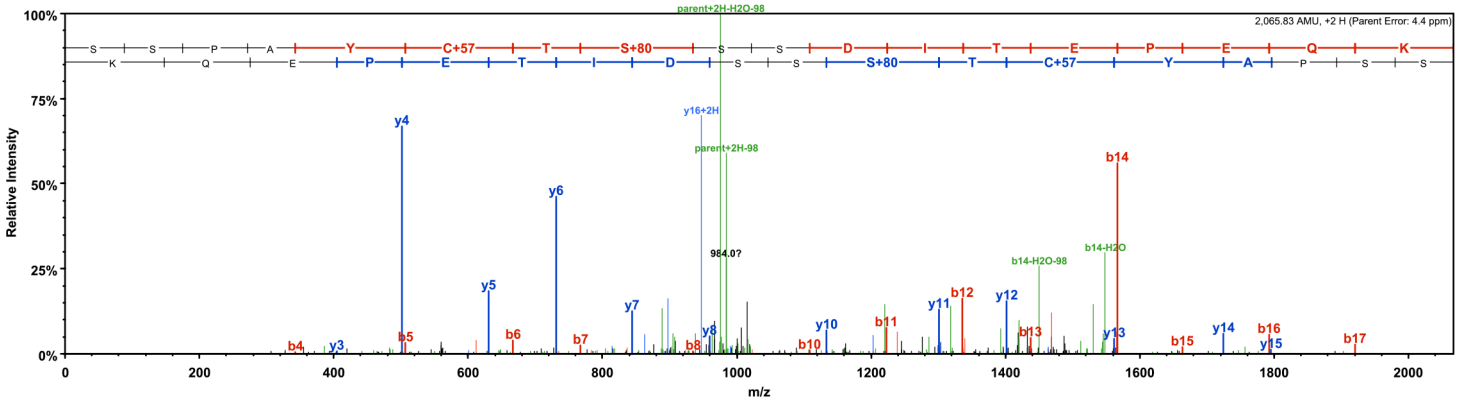

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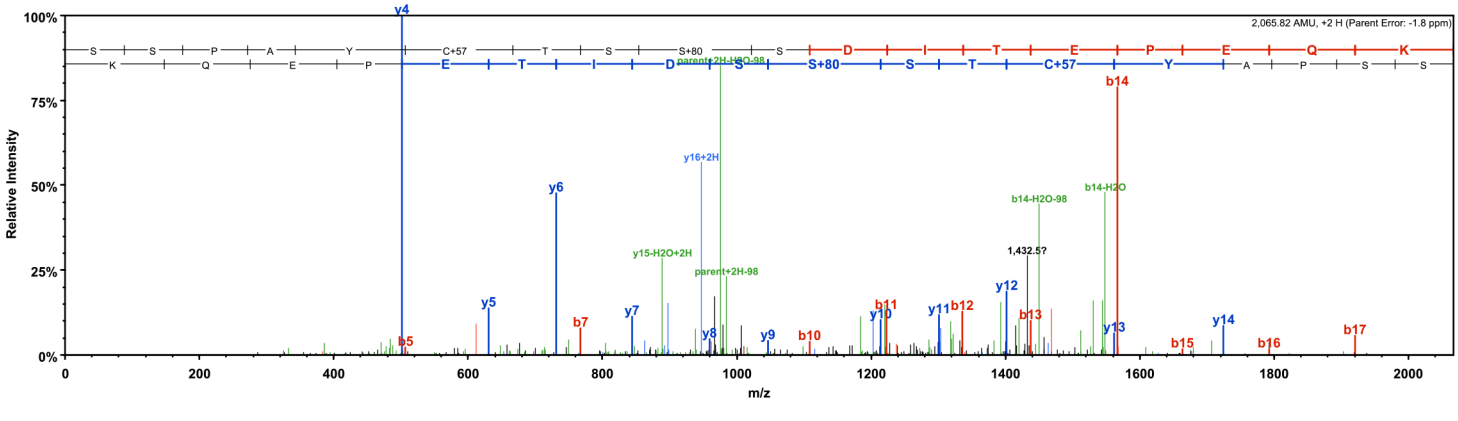

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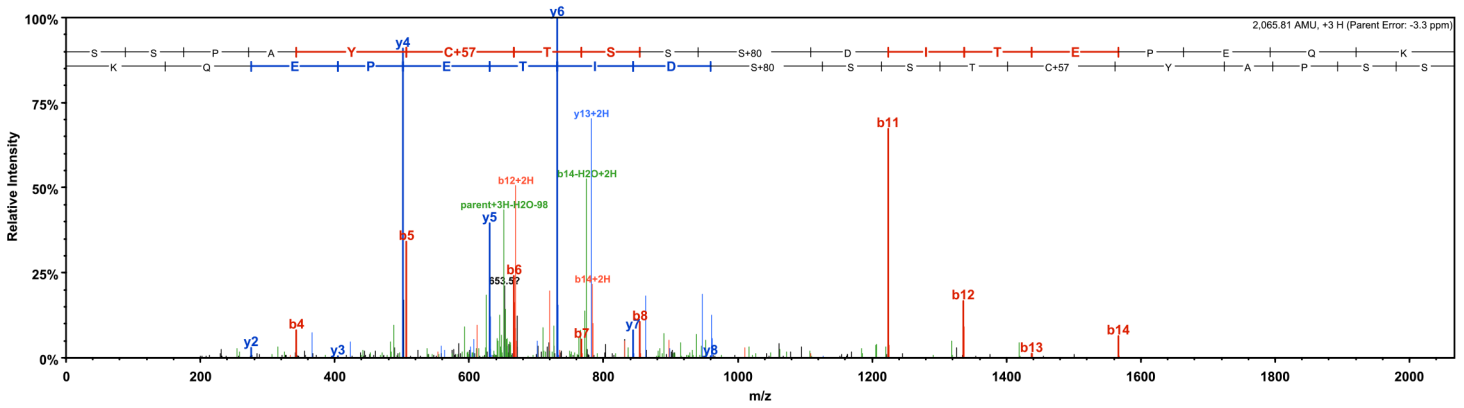
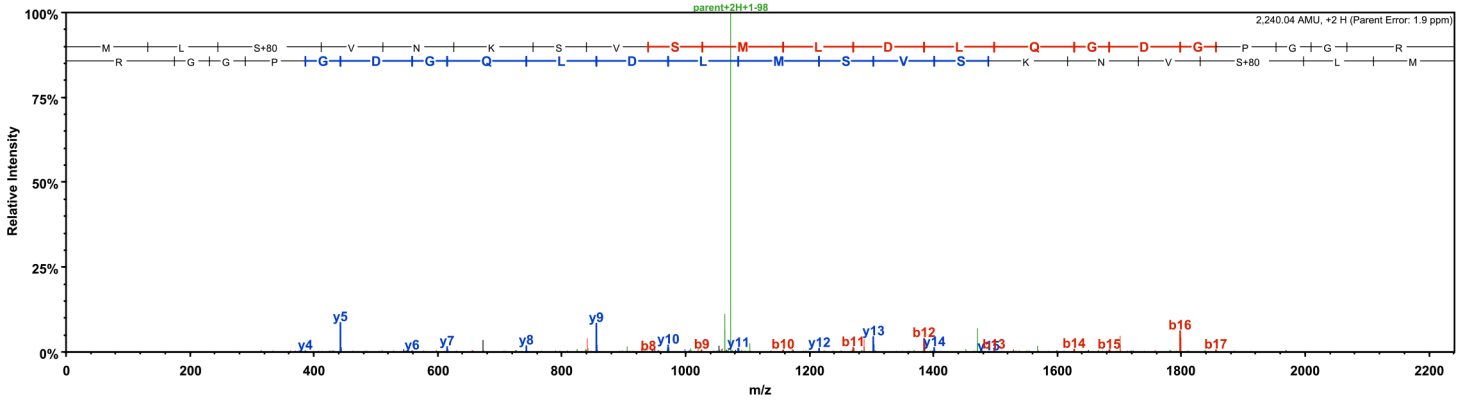
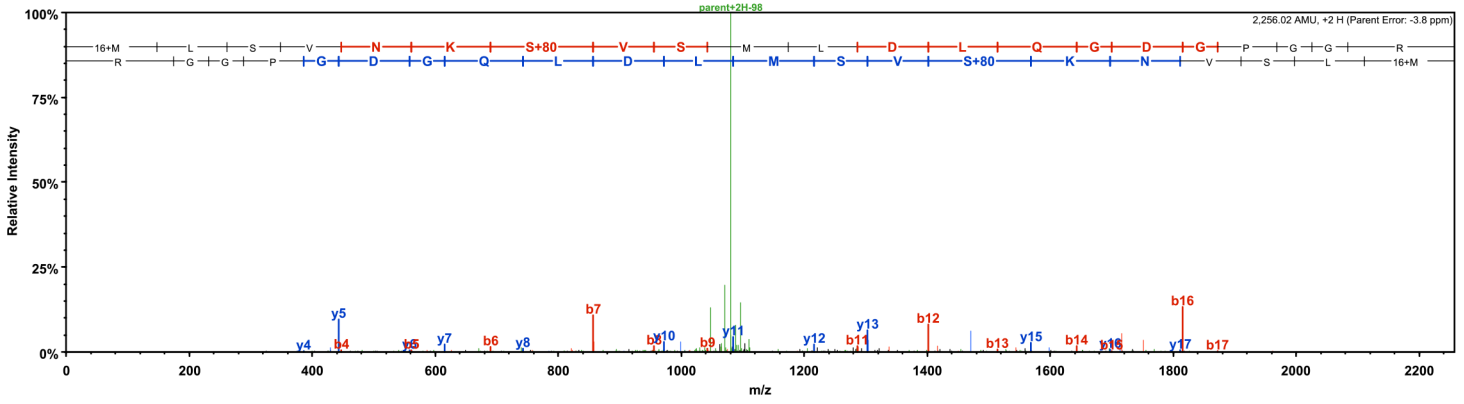


CaMKII S821 MS2



CaMKII S825 MS2



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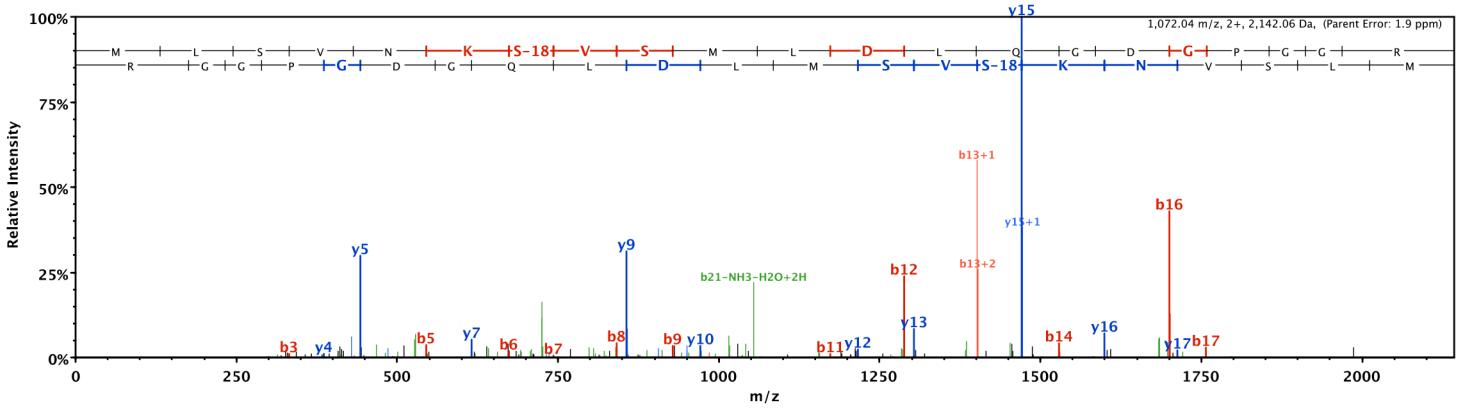

CaMKII S827

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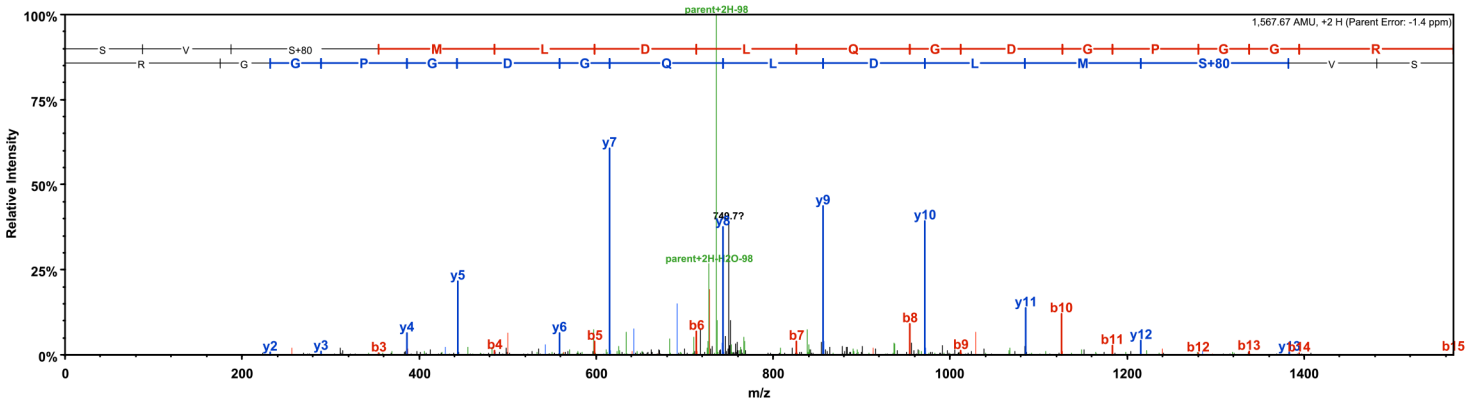

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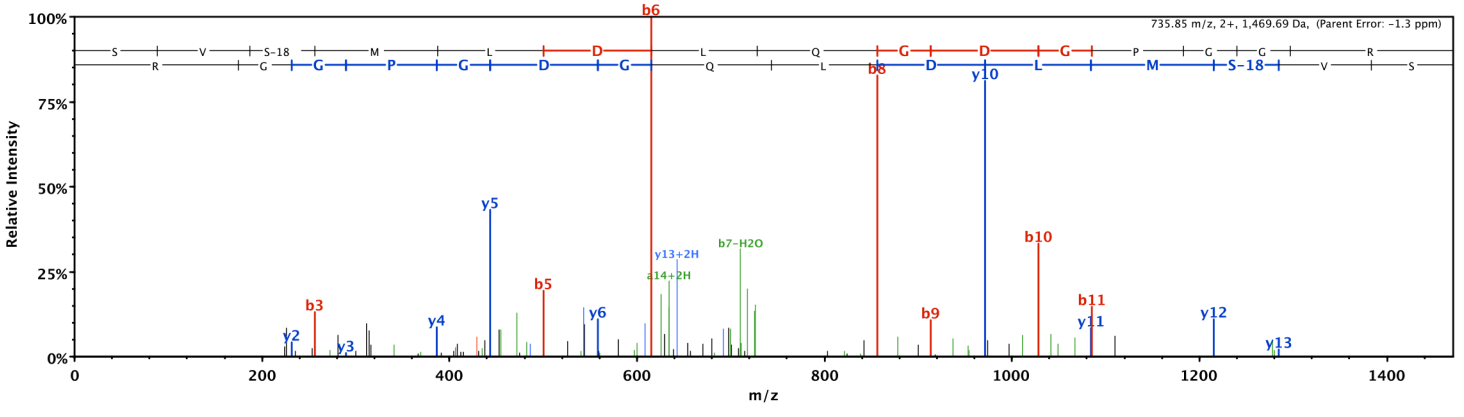

CaMKII S842

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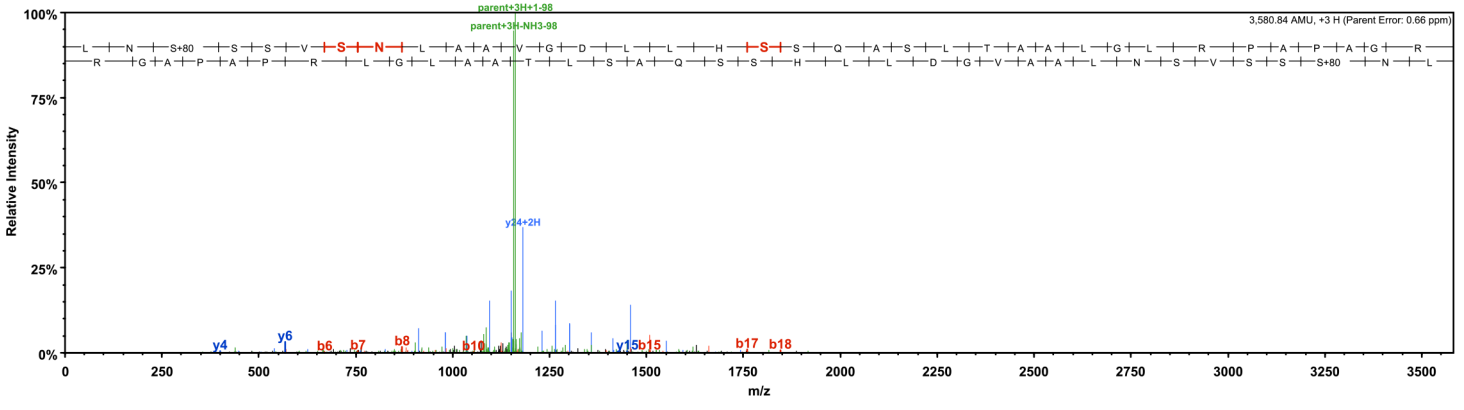

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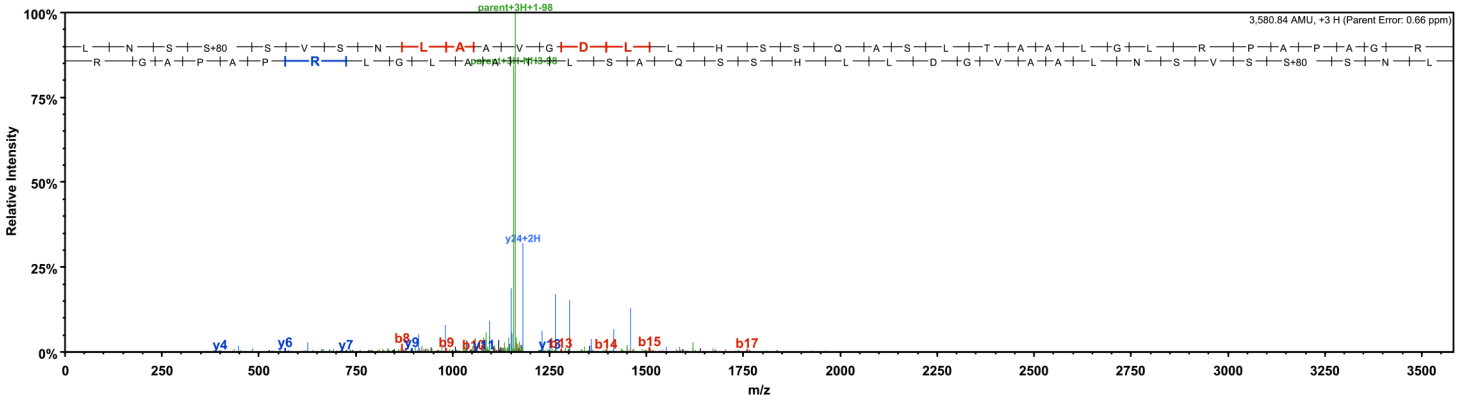

CaMKII S882

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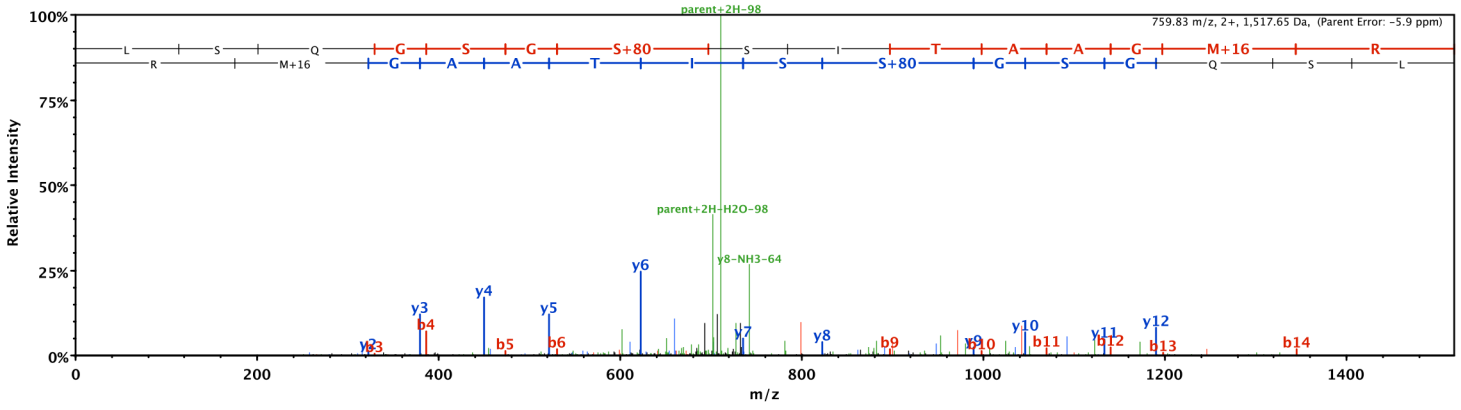

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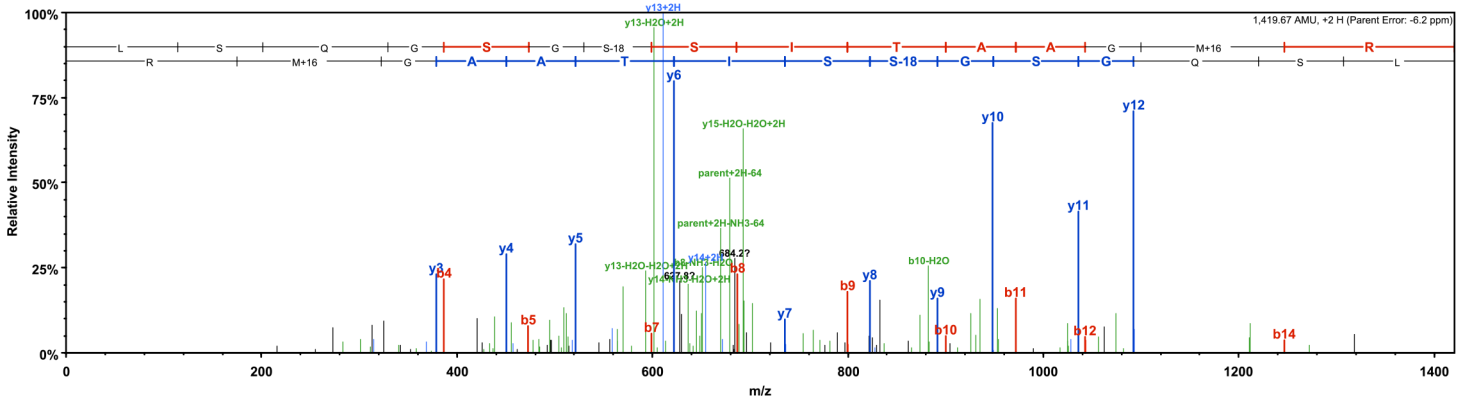

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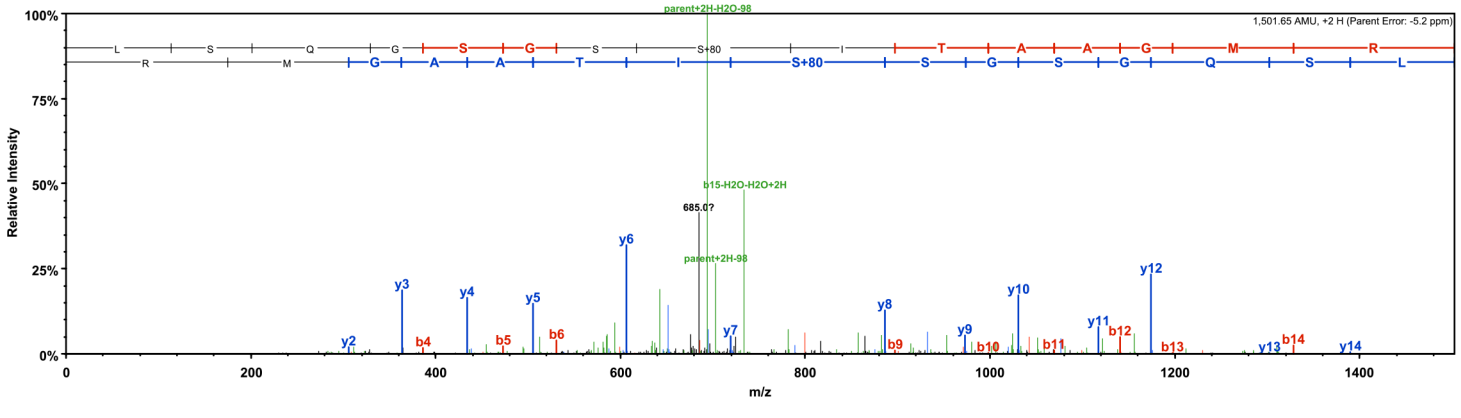

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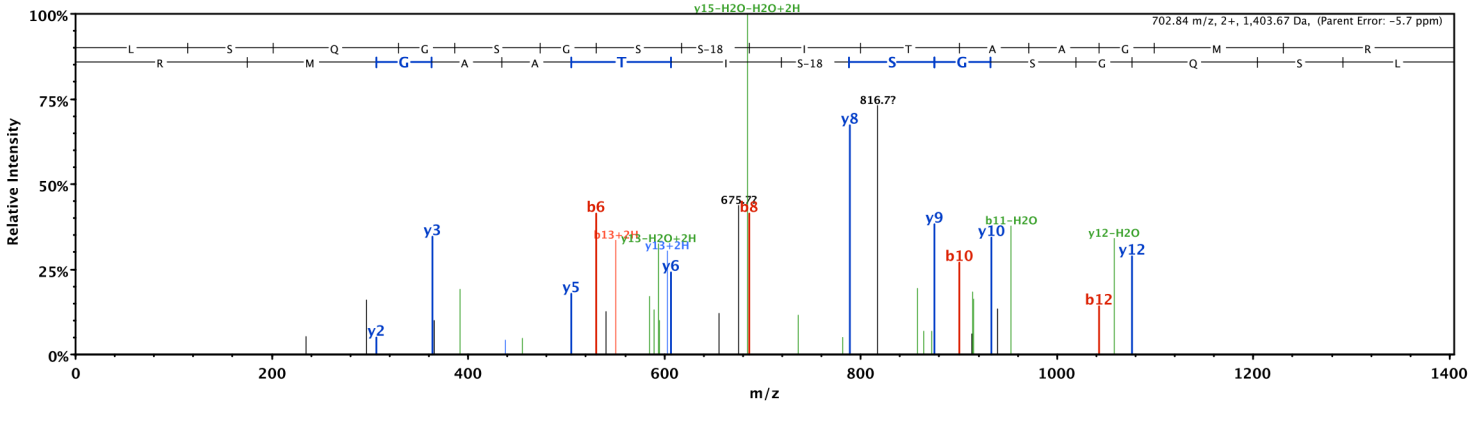

CaMKII T885

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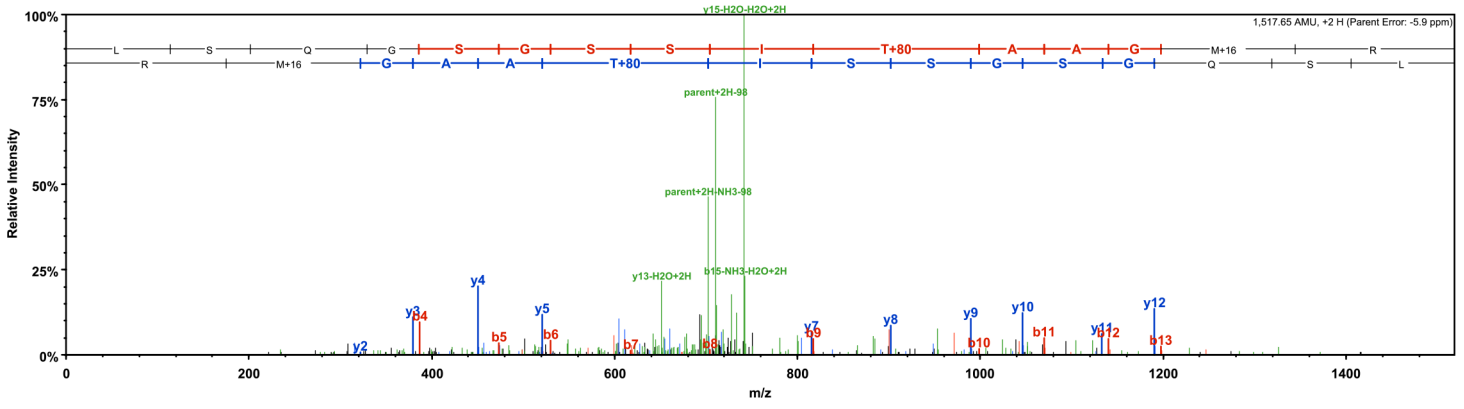

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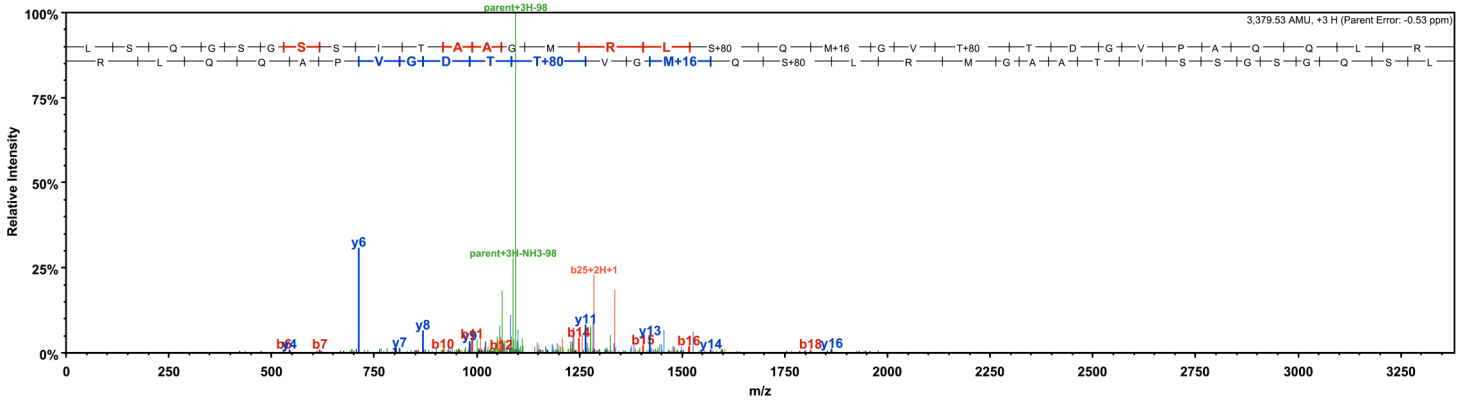

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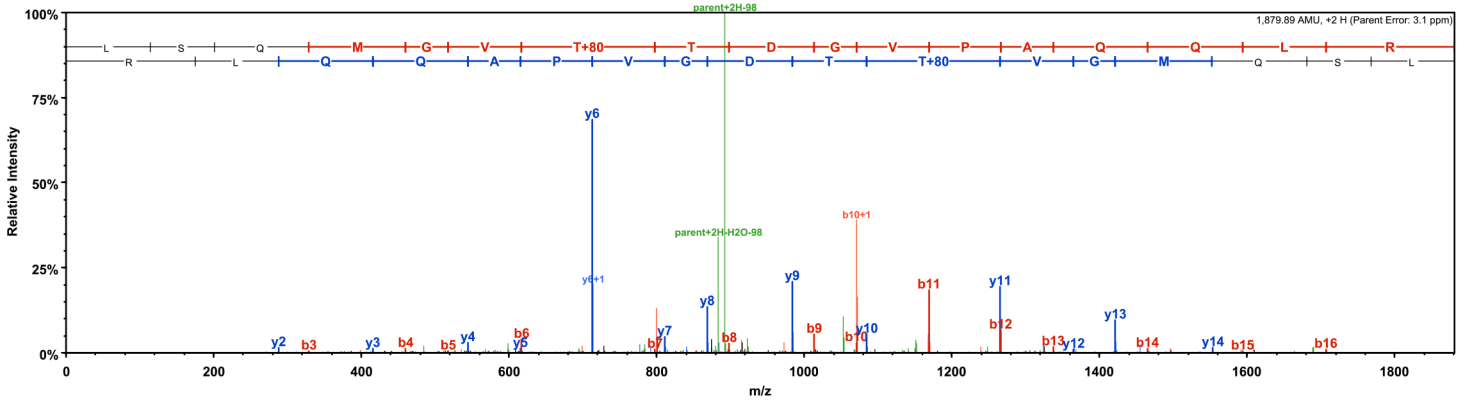

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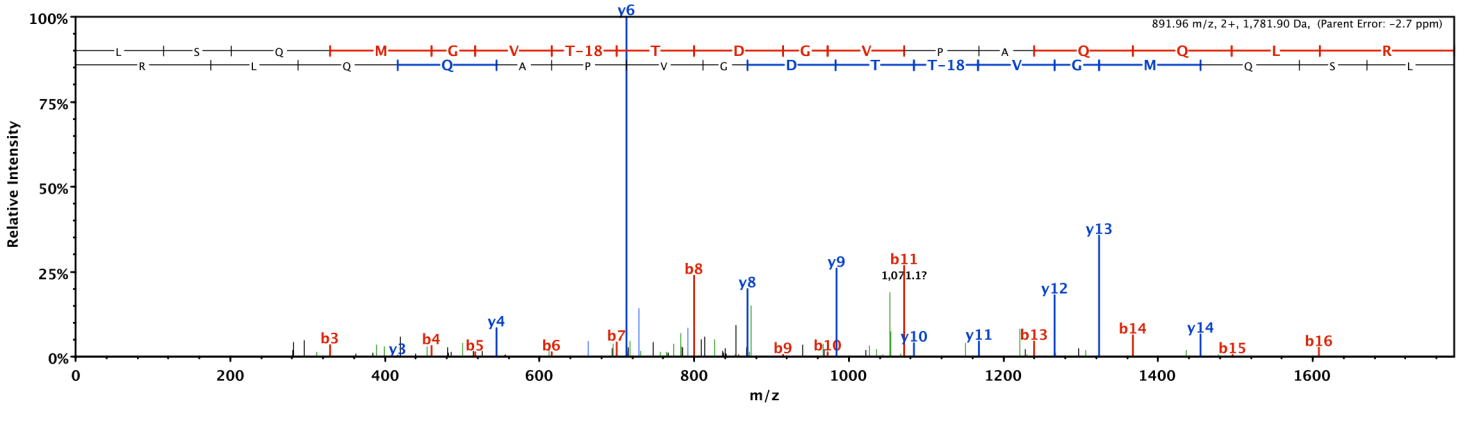

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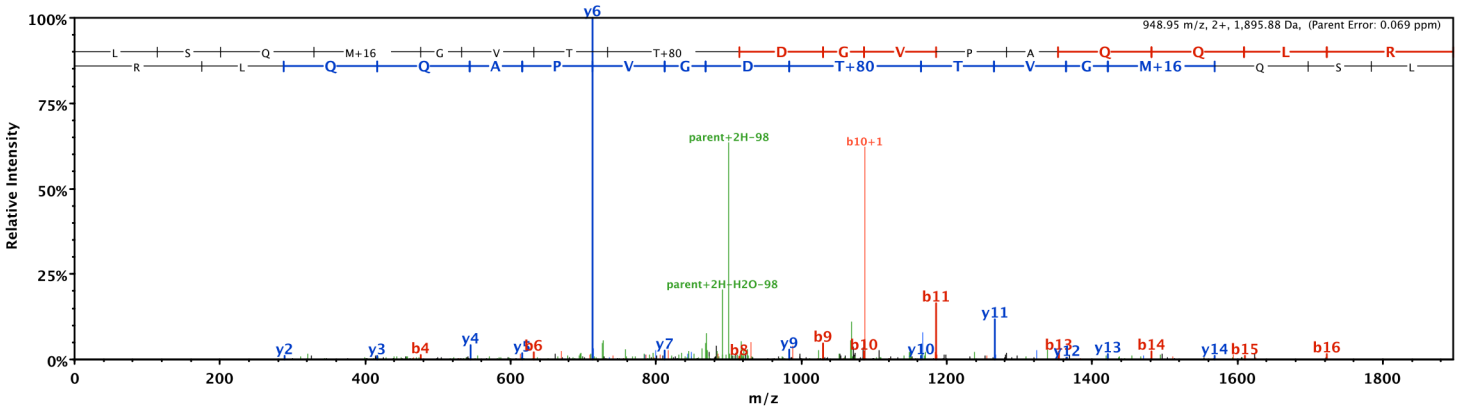

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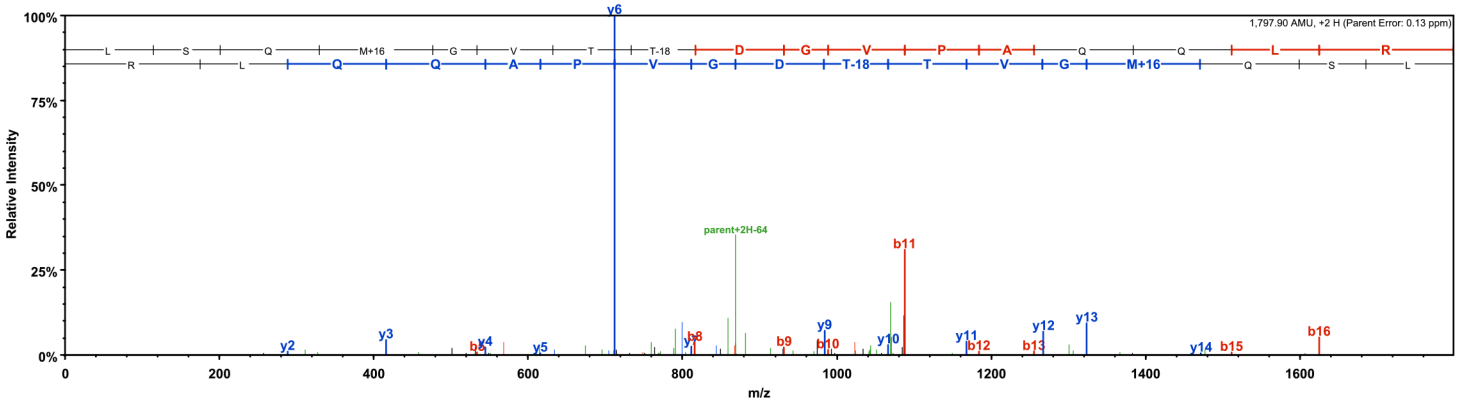

CaMKII S990

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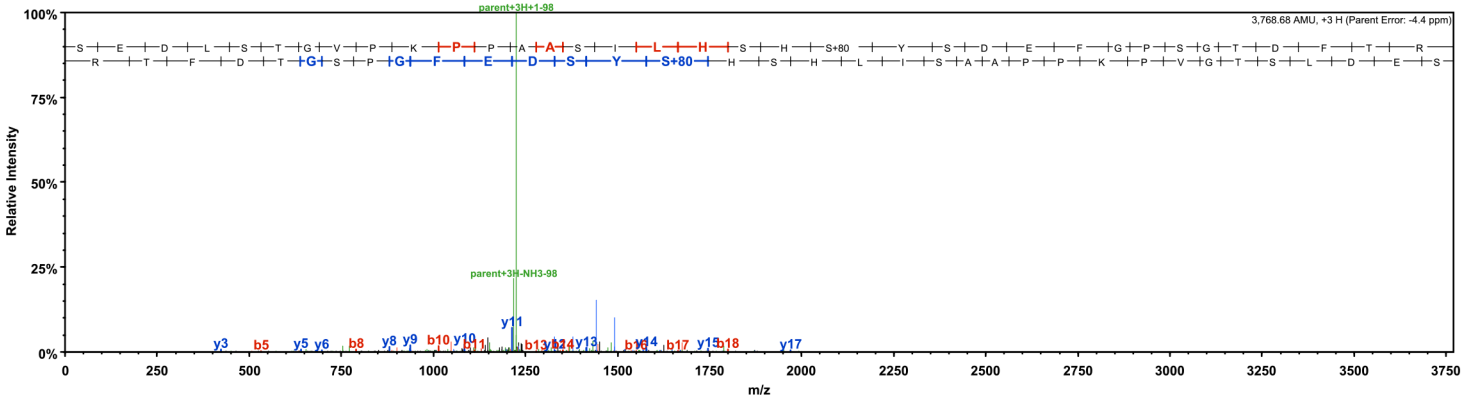

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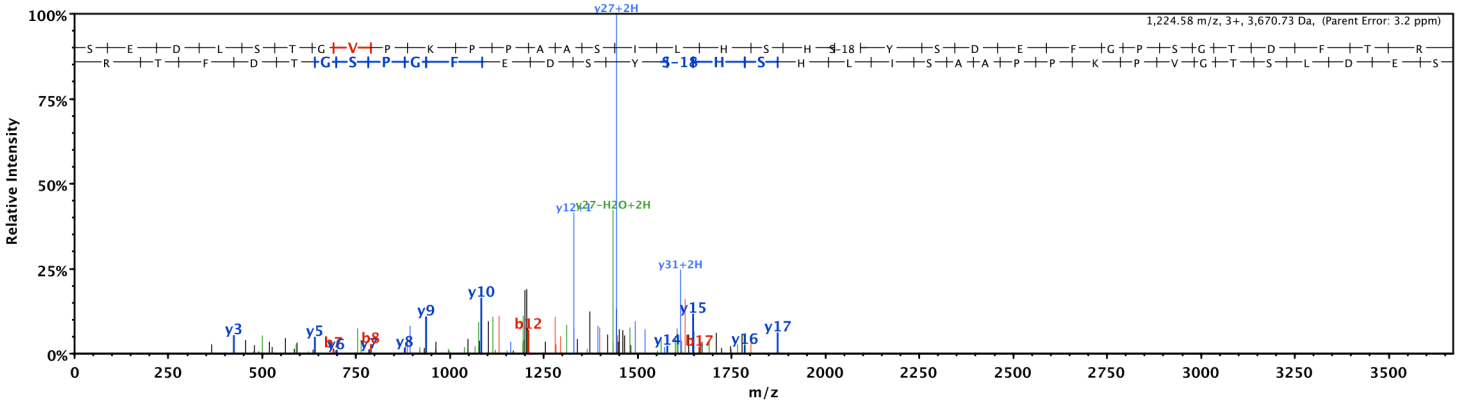
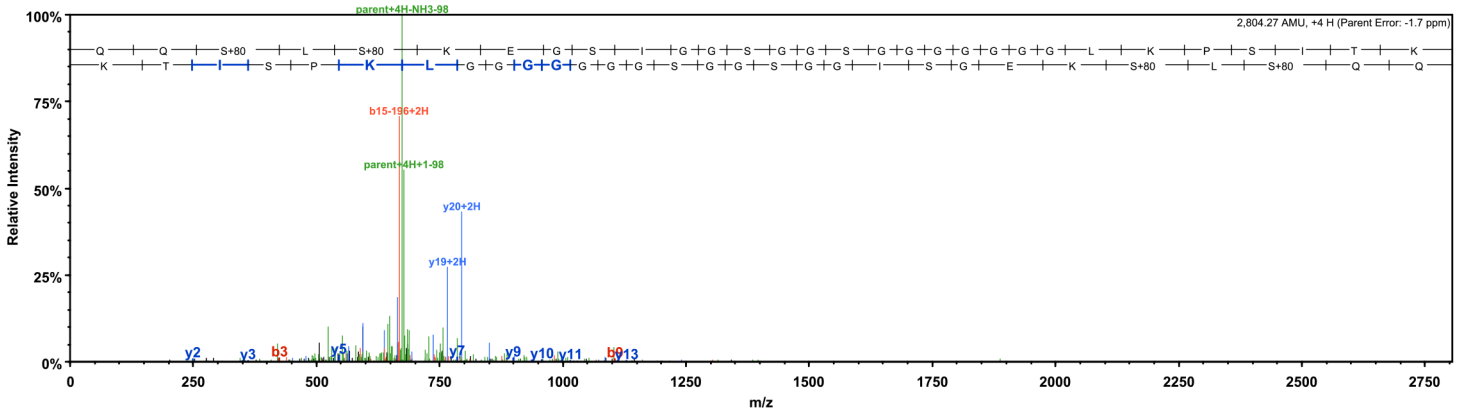


CaMKII S1093, S1095

MS2



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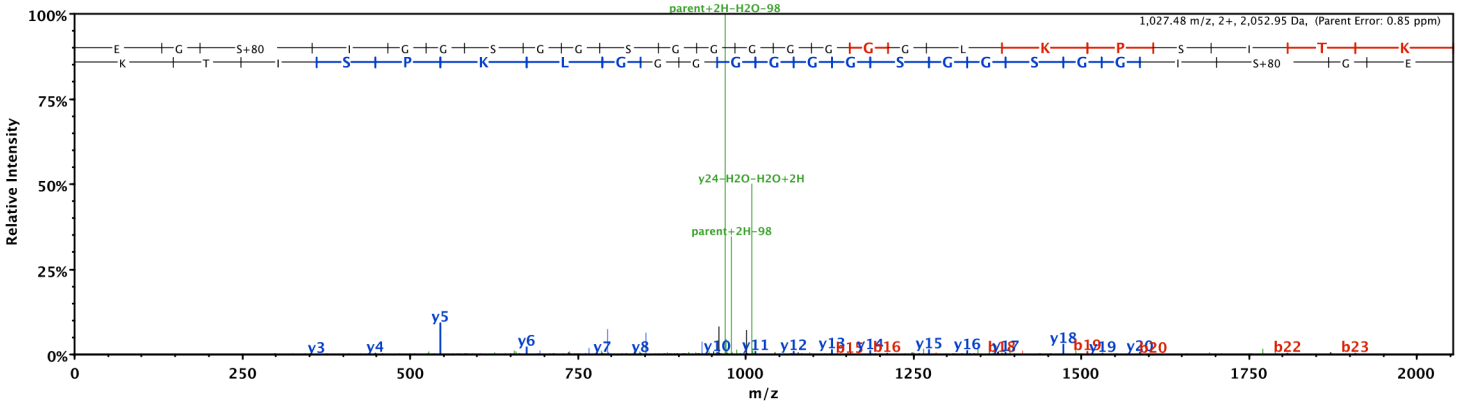

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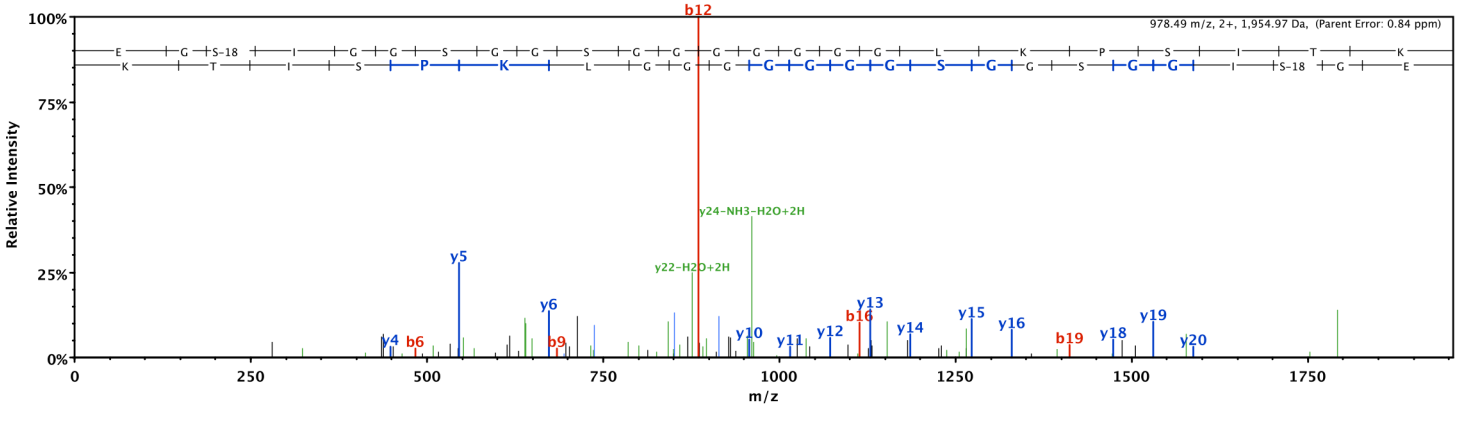

CaMKII S1123

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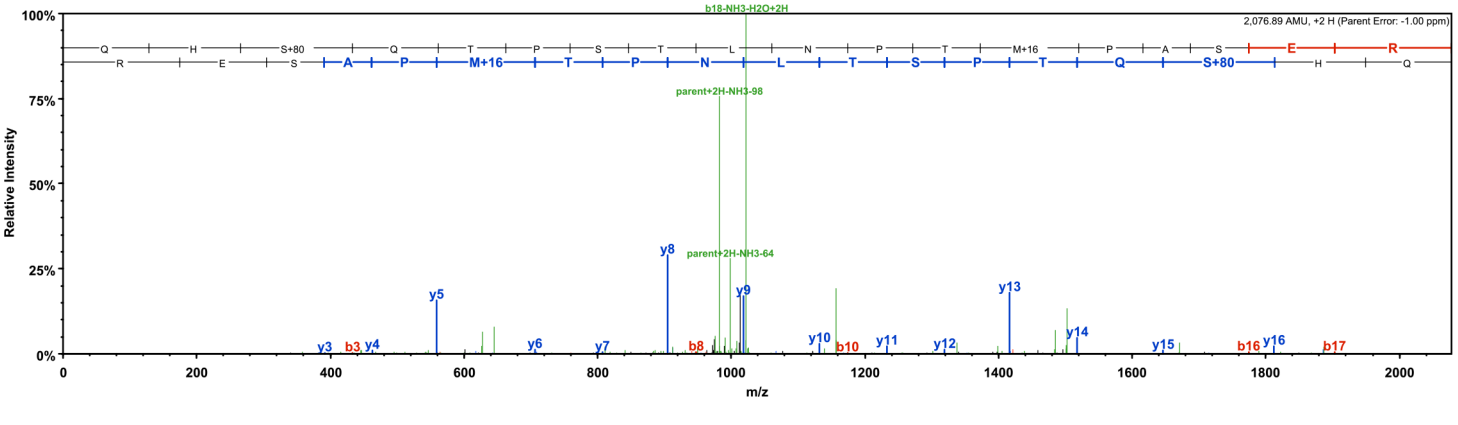

CaMKII S1150

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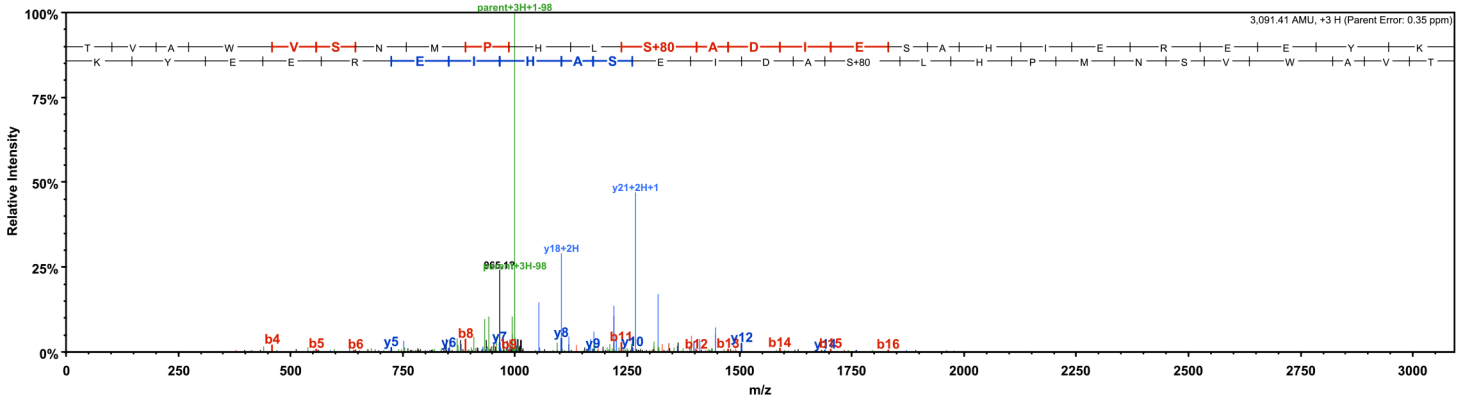

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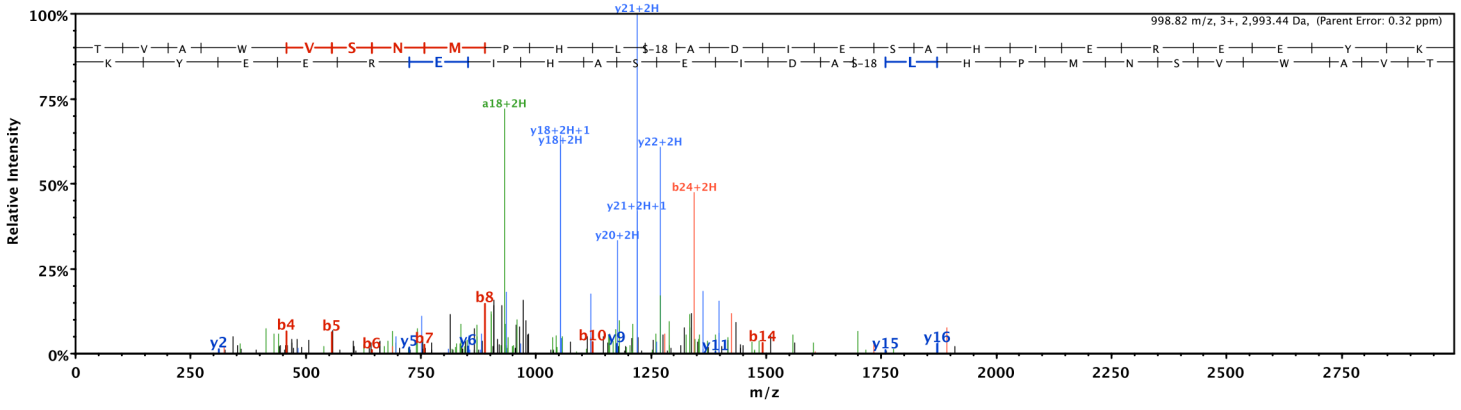

CaMKII S1171

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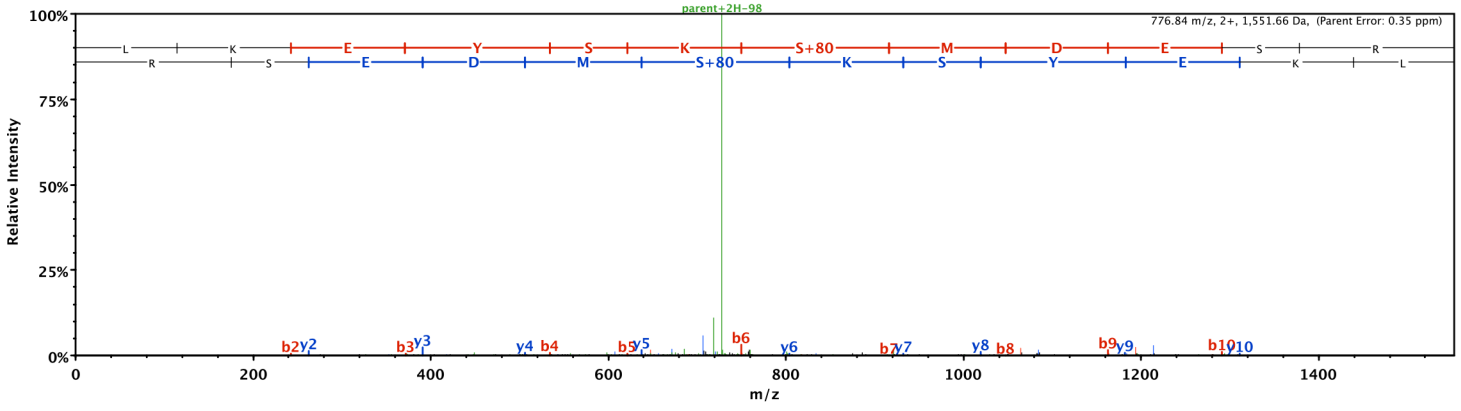

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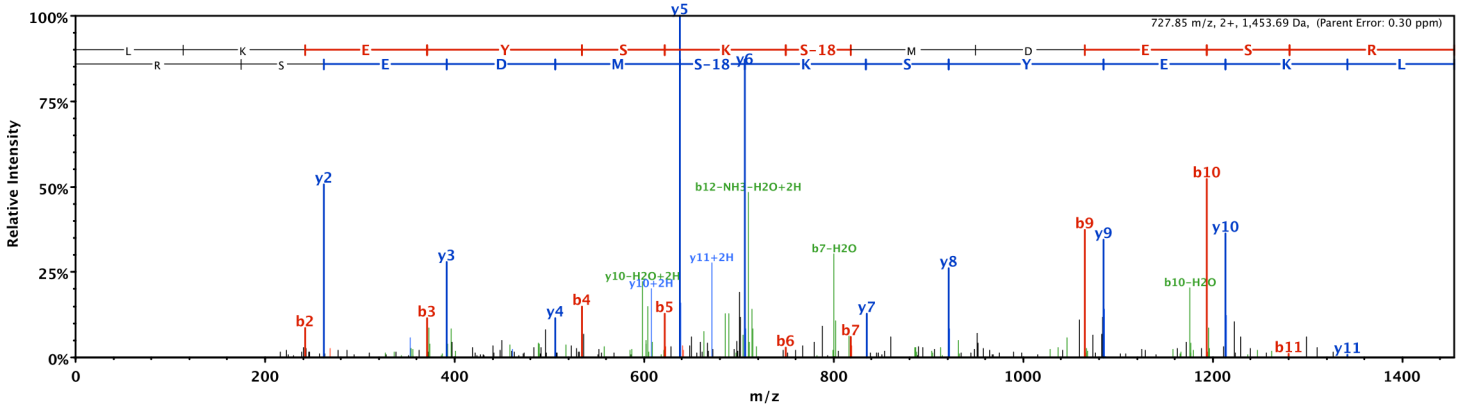

CaMKII S1210

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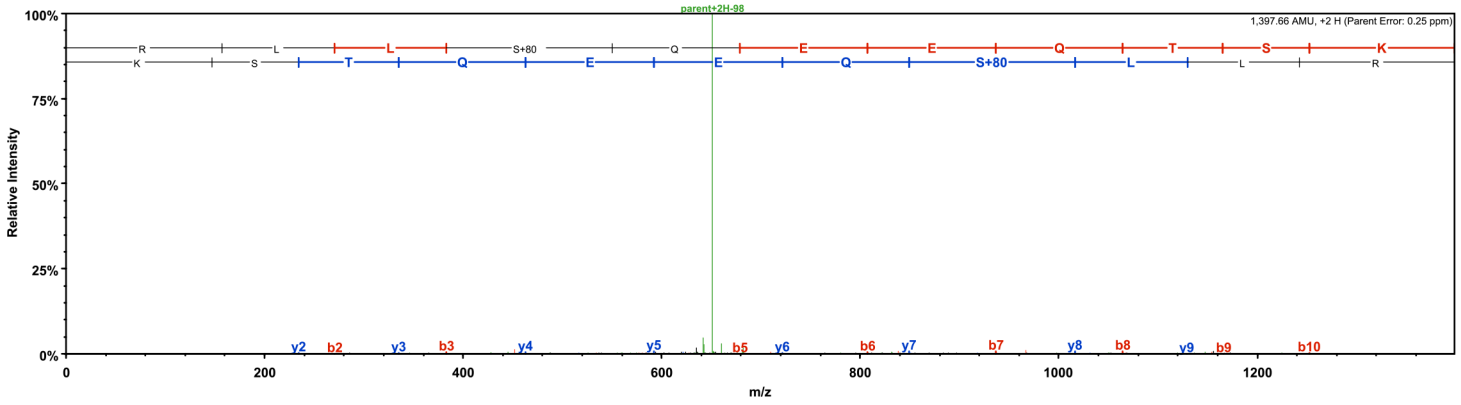

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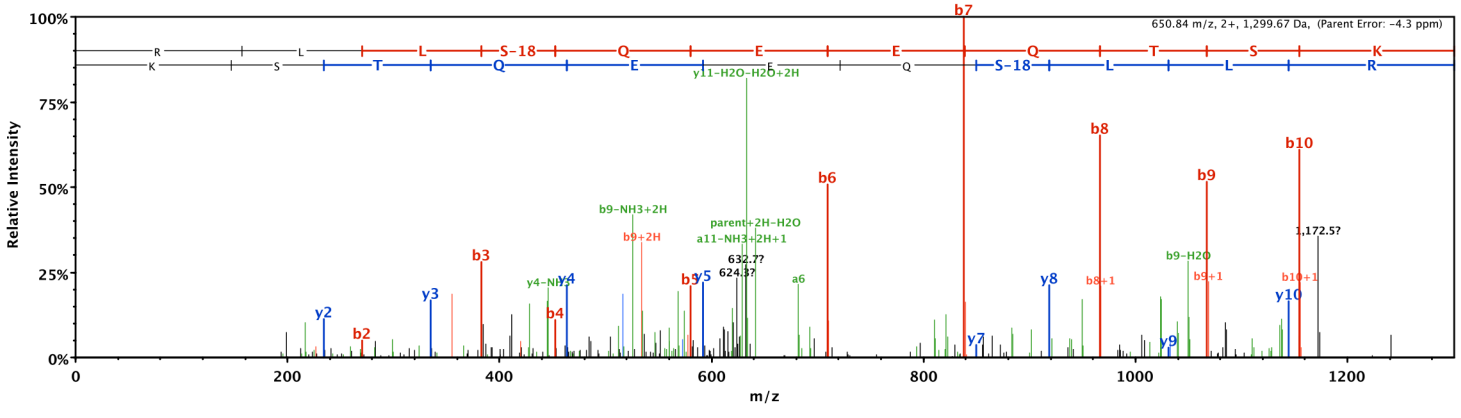

CaMKII S1283

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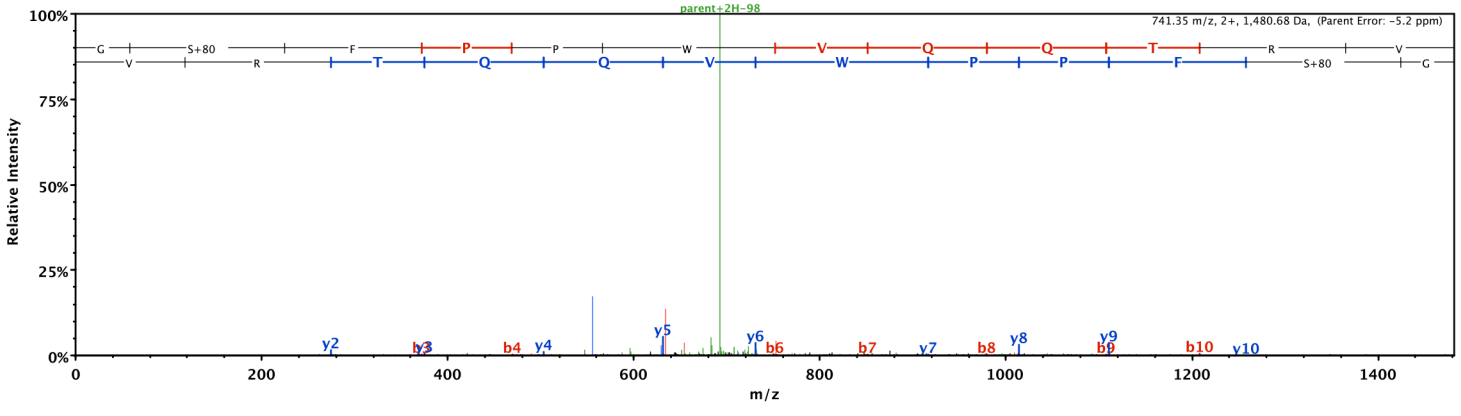

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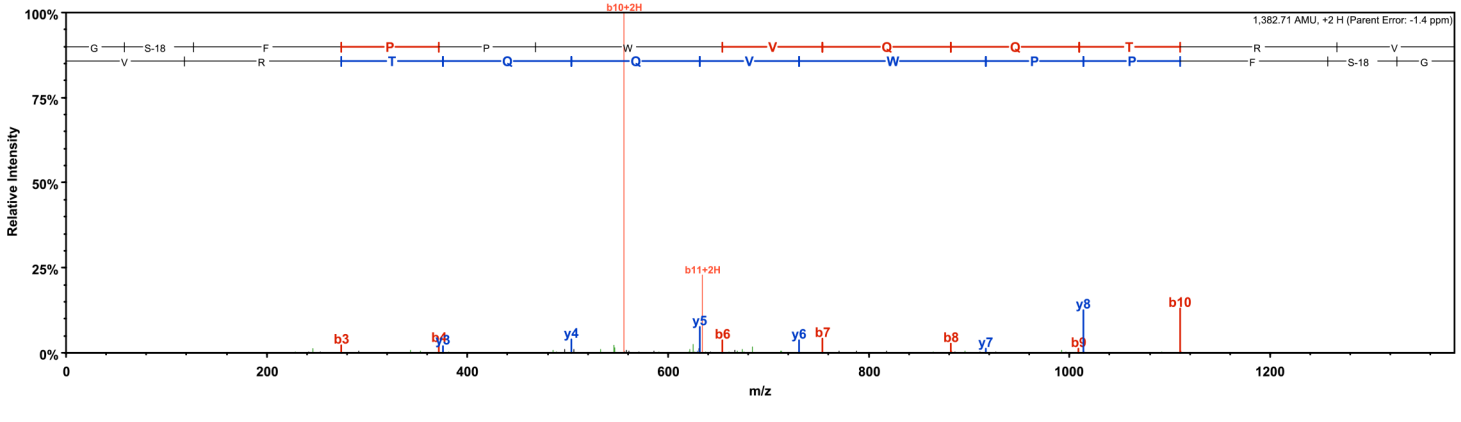

CaMKII T1291

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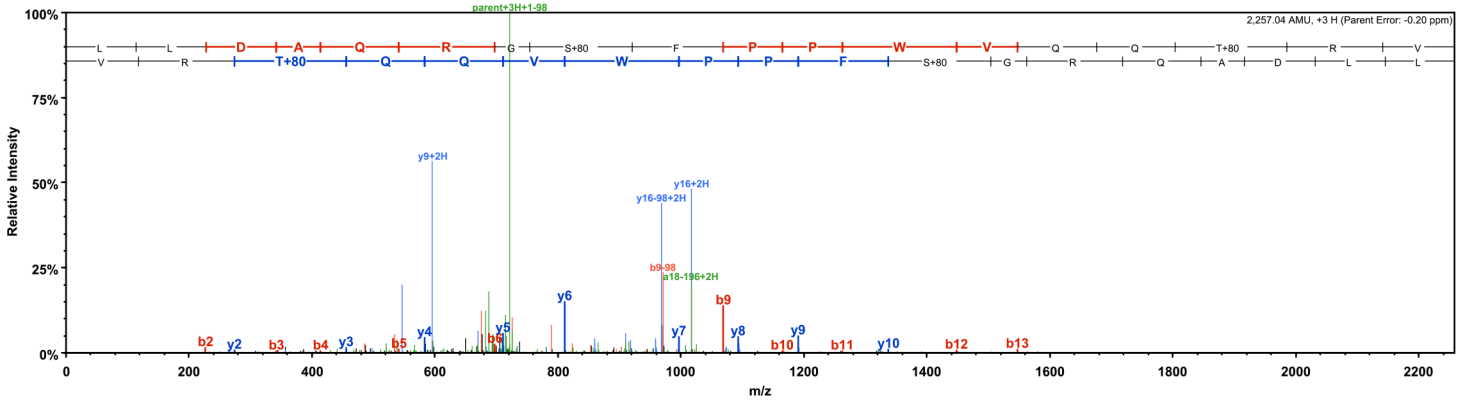

CDK5 S728

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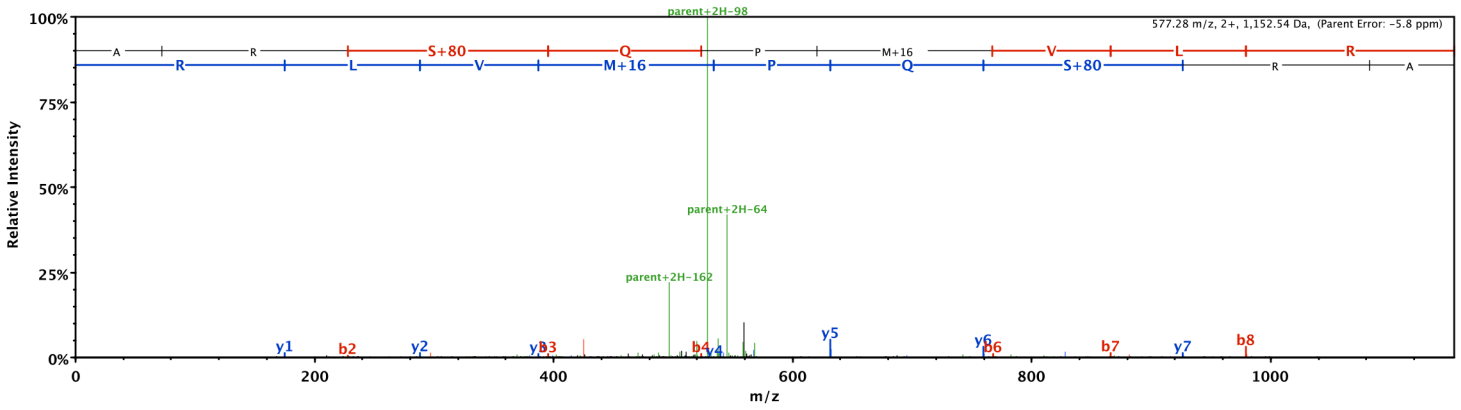

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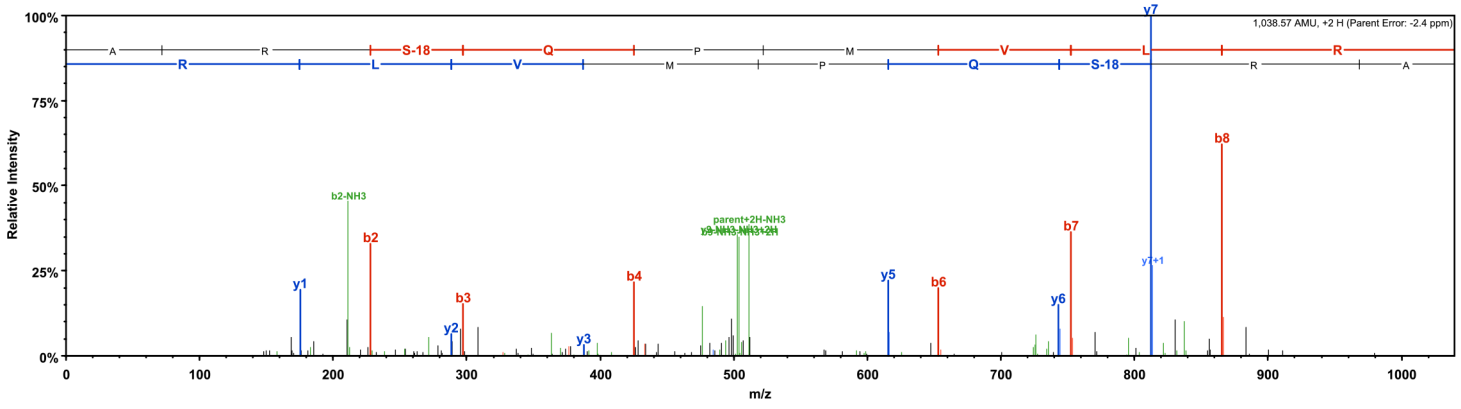

CDK5 S773

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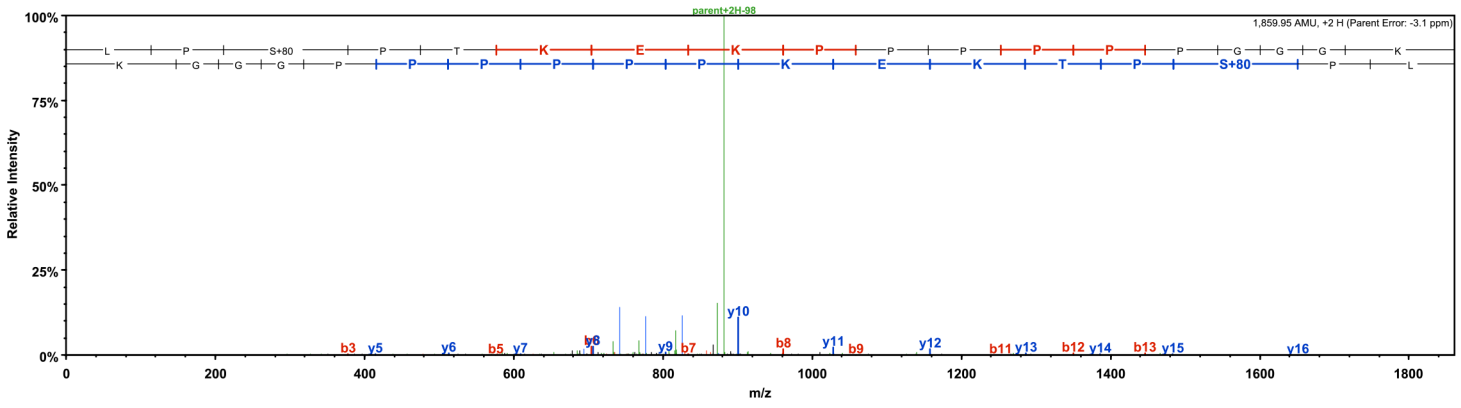
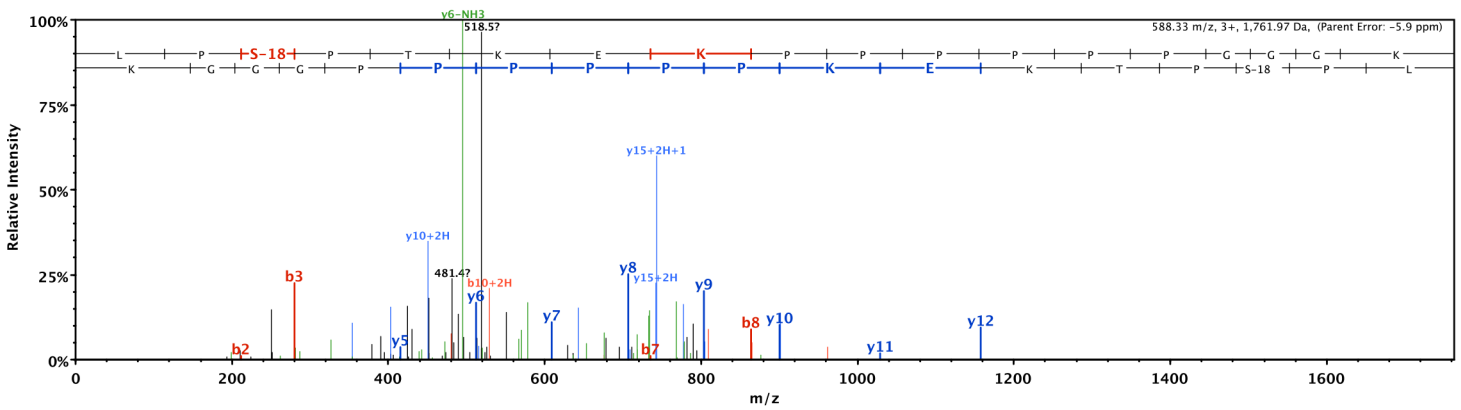


MS3



CDK5 T775

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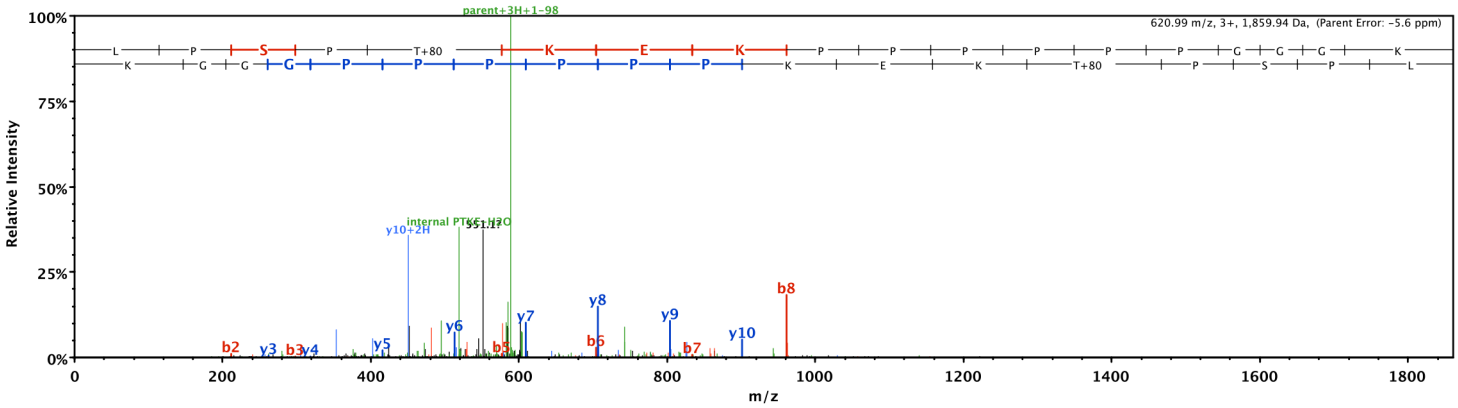
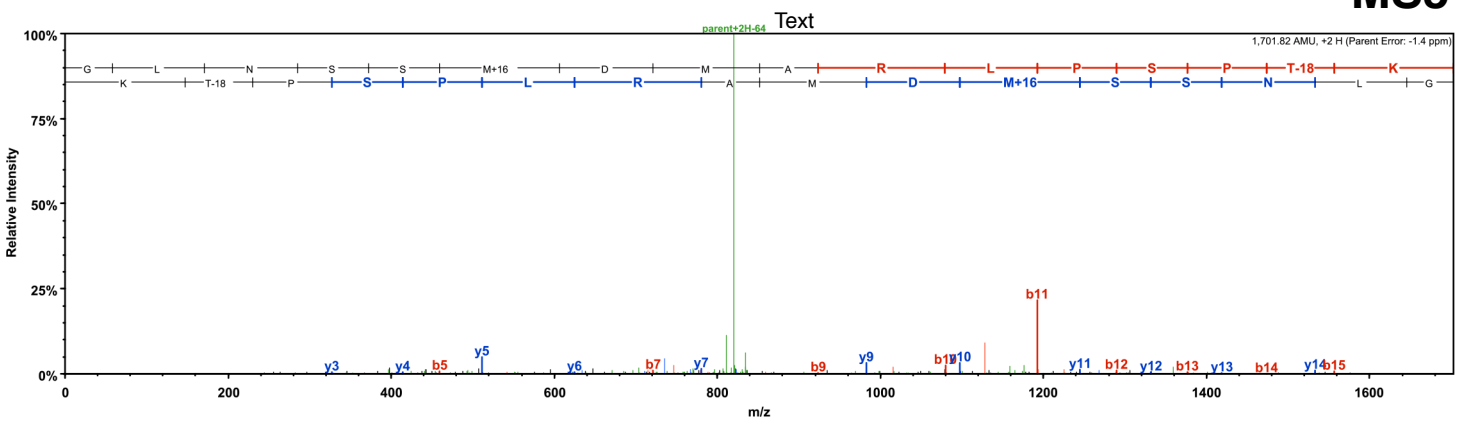


MS3



CDK5 S802

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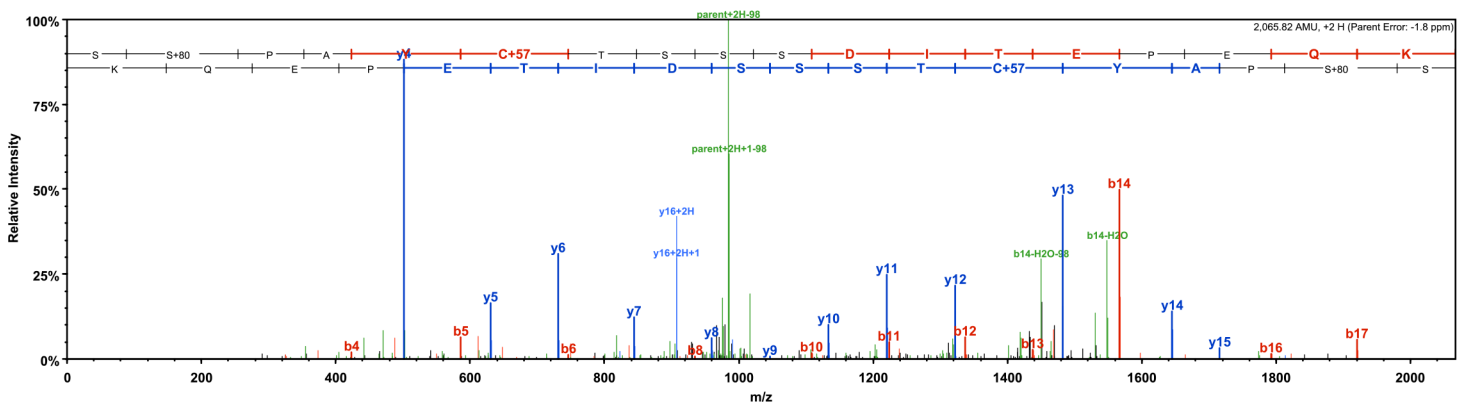
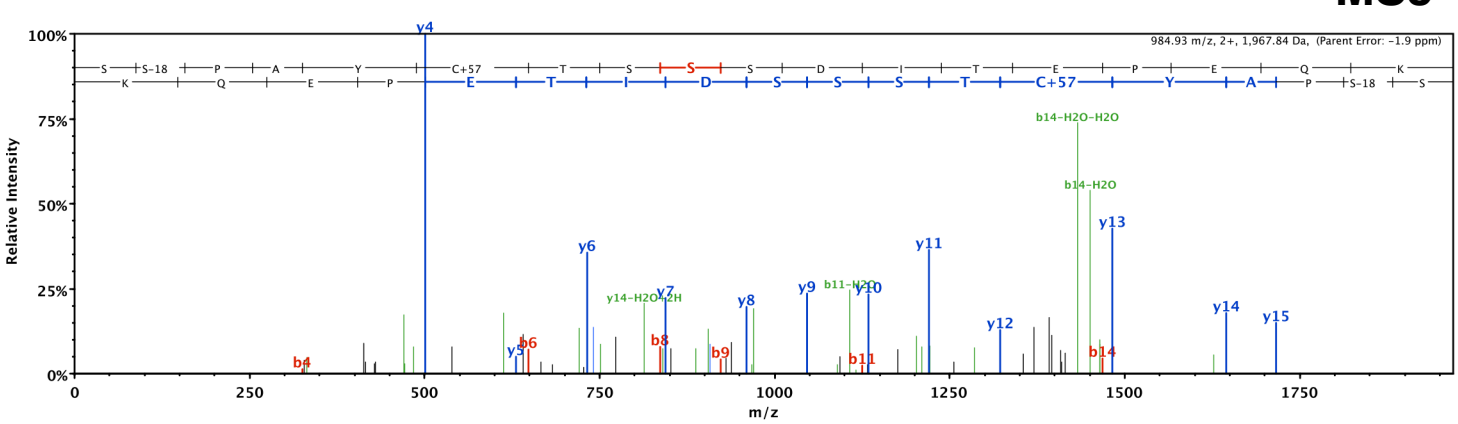


MS3



CDK5 S842

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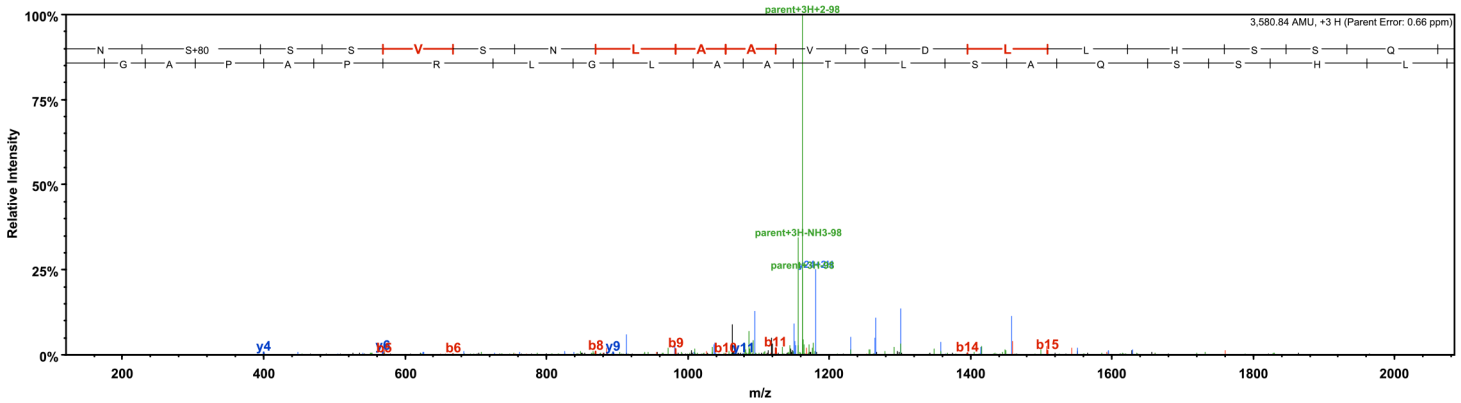

MS3